

0973297420300

SEQUENCE LISTING

<110> Cahoon, Edgar B.
<111> Cahoon, Rebecca E.

<120> Enzymes Involved In Petroselinic Acid Biosynthesis

<130> BB1413 US NA

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<150> 60/169,968
<151> 9 DECEMBER 1999

<160> 12

<170> Microsoft Office 97

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<211> 1344
<212> DNA
<213> Hedera helix

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<221> unsure
<222> (997)

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gataatctca aaatgtccgc aatcttcata gtcaactact ctatgccacc ccaaaagcta 240
gaaatattca agtccccgtga tgattggctt aggaacaatg tggtgatca cttcaaatc 300
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gcatggactg ccaagagaga tagatcatgtt gacccatccataa ataaatgttccat 600
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gatatacaatg cagaaaaacaccccttacatgc ggtttcatctt acatccatctt ccaagagaga 720
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tggatgttca atccggatggatcg gggatggatcg aacggatggatcg aaggaaatgtt acgacccatcg 1260
gatgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgttgcgtt 1320
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<211> 394
<212> PRT
<213> Hedera helix

<220>

<221> UNSURE
<222> (318)

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Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
35 40 45
Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
50 55 60
Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
65 70 75 80
Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
85 90 95
Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg
100 105 110
Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
115 120 125
Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
130 135 140
Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
145 150 155 160
Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
165 170 175
Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
180 185 190
Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
195 200 205
Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
210 215 220
Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
225 230 235 240
Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
245 250 255
Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
260 265 270
Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
275 280 285
Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
290 295 300

Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Xaa Val Tyr
 305 310 315 320
 Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp
 325 330 335
 Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln
 340 345 350
 Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys
 355 360 365
 Val Gln Gly Lys Glu Lys Lys Lys Ala Glu His Pro Val Ser Phe
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 Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile
 385 390
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 <213> Hedera helix
 <400> 3
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 catcgattc cttcacctct atcgcaagct ccctcaagca aaaccaggga cttgccaaga 180
 gttcatttc acttcgttgc aatggcaat cttccgttcc acttaggtt ctgtcggoac 240
 cacttcgtt cagagtgtca tgccgcgca aaccaggcac agtggacaaag gtgtgtqaga 300
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 cagcgttgc ggctgttct ctgcgcacgg ttgagatgt gatggacta aaggaggaaat 420
 tcggaaatca gctgtggaaa aaga 445
 <210> 4
 <211> 114
 <212> PRT
 <213> Hedera helix
 <400> 4
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 20 25 30
 Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
 35 40 45
 Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
 50 55 60
 Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Leu Ile Leu Gln Val
 65 70 75 80
 Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
 85 90 95
 Val Glu Ile Val Met Gly Leu Lys Glu Glu Phe Gly Ile Lys Arg Gly
 100 105 110

00802F-2652E<60

Lys Lys
114

<210> 5
<211> 920
<212> DNA
<213> Hedera helix

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catcgatcc ctccacccct atcgcaagct ccctcaagoa aaaccaggaa ctggccaaga 180
gttcaatttctc actctctgtc aatggaaat cttccgttc acttaggttgc ctgtcgccac 240
cacttcgtttt cagagtgtca tgccgcagcga aaccagcgcac agtggacaag gtgtgigaga 300
ttgtgcggaa aacaatggcg ctgcgcgcgtt attcgcgtt cactggagag tc当地atcg 360
cagcgcgttgg ggctgttattt ctcgcacccgtt tttggattgtt gatggacta gaggaggaaat 420
tcgaaatcg cgtggaaagaa gaaatgtc acgaccatggcactgttcaa gatgcacccg 480
acatgttgc aagacttgtt gaaaaaaagg agttagaaagaa ccggggtagaa aattctgc 540
aataatggattt ttaaggacatc ttactttttt ataggatgtt atcaagactt tcattaccc 600
acatgttattt tttatgtatcctt catggacccg caaaatgtt agtggatgtt aaatttttaccc 660
cgagtcgttcc ctctttatattt caaaatgtt gaggccggaa aagaggctat gctatctc 720
atctcgatcc ttttttttt ctgtcgccatc ttctgttgg agtggatgtt ttttatctaa 780
acatgttgc tttttttttt aaaaatgtt caaaaaatata tatcttggtt ttgagatgtt 840
ttggatgtt gctcttgata ttttgaatgtt attttggatgtt attcaaaaaaaa aaaaaaaaaa 900
aaaaaaaaaaa aaaaaaaaaaaa 920

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<212> PRT
<213> Hedera helix

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Val Asn Gly Lys Ser Phe Arg Ser Leu Arg Leu Leu Ser Ala Pro Leu
35 40 45

Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Ala Thr Val Asp Lys Val
50 55 60

Cys Glu Ile Val Arg Lys Gln Leu Ala Leu Pro Ala Asp Ser Ala Val
65 70 75 80

Thr Gly Glu Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
85 90 95

Val Glu Ile Val Met Gly Leu Glu Glu Asp Phe Gly Ile Ser Val Glu
100 105 110

Glu Glu Ser Ala Gln Thr Ile Ala Thr Val Gin Asp Ala Ala Asp Leu
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Ile Glu Lys Leu Val Glu Lys Lys Glu
130 135

<210> 7
 <211> 385
 <212> PRT
 <213> Coriandrum sativum

<400> 7
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 Asn Met Phe Thr Arg Ile Ala Pro Pro Gln Ala Gly Arg Val Arg Ser
 20 25 30
 Lys Val Ser Met Ala Ser Thr Leu His Ala Ser Pro Leu Val Phe Asp
 35 40 45
 Lys Leu Lys Ala Gly Arg Pro Glu Val Asp Glu Leu Phe Asn Ser Leu
 50 55 60
 Glu Gly Trp Ala Arg Asp Asn Ile Leu Val His Leu Lys Ser Val Glu
 65 70 75 80
 Asn Ser Trp Gln Pro Gln Asp Tyr Leu Pro Asp Pro Thr Ser Asp Ala
 85 90 95
 Phe Glu Asp Gln Val Lys Glu Met Arg Glu Arg Ala Lys Asp Ile Pro
 100 105 110
 Asp Glu Tyr Phe Val Val Leu Val Gly Asp Met Ile Thr Glu Glu Ala
 115 120 125
 Leu Pro Thr Tyr Met Ser Met Leu Asn Arg Cys Asp Gly Ile Lys Asp
 130 135 140
 Asp Thr Gly Ala Gln Pro Thr Ser Trp Ala Thr Trp Thr Arg Ala Trp
 145 150 155 160
 Thr Ala Glu Glu Asn Arg His Gly Asp Leu Leu Asn Lys Tyr Leu Tyr
 165 170 175
 Leu Ser Gly Arg Val Asp Met Arg Met Ile Glu Lys Thr Ile Gln Tyr
 180 185 190
 Leu Ile Gly Ser Gly Met Asp Thr Lys Thr Glu Asn Cys Pro Tyr Met
 195 200 205
 Gly Phe Ile Tyr Thr Ser Phe Gln Glu Arg Ala Thr Phe Ile Ser His
 210 215 220
 Ala Asn Thr Ala Lys Leu Ala Gln His Tyr Gly Asp Lys Asn Leu Ala
 225 230 235 240
 Gln Val Cys Gly Asn Ile Ala Ser Asp Glu Lys Arg His Ala Thr Ala
 245 250 255
 Tyr Thr Lys Ile Val Glu Lys Leu Ala Glu Ile Asp Pro Asp Thr Thr
 260 265 270
 Val Ile Ala Phe Ser Asp Met Met Arg Lys Lys Ile Gln Met Pro Ala
 275 280 285

His Ala Met Tyr Asp Gly Ser Asp Asp Met Leu Phe Lys His Phe Thr
 290 295 300
 Ala Val Ala Gln Gln Ile Gly Val Tyr Ser Ala Trp Asp Tyr Cys Asp
 305 310 315 320
 Ile Ile Asp Phe Leu Val Asp Lys Trp Asn Val Ala Lys Met Thr Gly
 325 330 335
 Leu Ser Gly Glu Gly Arg Lys Ala Gln Glu Tyr Val Cys Ser Leu Ala
 340 345 350
 Ala Lys Ile Arg Arg Val Glu Glu Lys Val Gln Gly Lys Glu Lys Lys
 355 360 365
 Ala Val Leu Pro Val Ala Phe Ser Trp Ile Phe Asn Arg Gln Ile Ile
 370 375 380
 Ile
 385
 <210> 8
 <211> 137
 <212> PRT
 <213> Coriandrum sativum
 <400> 8
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 20 25 30
 Ala Lys Ala Lys Ser Phe Gly Ala Leu Thr Leu Arg Asn Ala Pro Leu
 35 40 45
 Arg Phe Arg Val Ser Cys Ala Ala Lys Pro Glu Thr Val Glu Lys Val
 50 55 60
 Cys Glu Ile Val Lys Lys Gln Leu Ala Leu Pro Pro Thr Thr Glu Val
 65 70 75 80
 Ser Gly Asp Ser Lys Phe Ala Ala Leu Gly Ala Asp Ser Leu Asp Thr
 85 90 95
 Val Glu Ile Val Met Gly Leu Glu Glu Phe Gly Ile Ser Val Glu
 100 105 110
 Glu Glu Ser Ala Gln Ala Ile Ala Thr Val Gln Asp Ala Ala Asp Leu
 115 120 125
 Ile Glu Lys Leu Cys Glu Lys Lys Glu
 130 135
 <210> 9
 <211> 1381
 <212> DNA
 <213> Hedera helix

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 aagaagaacc accctgtc当地 gtttgc当地 taaccatcag tggccatc当地 agtttagtct 180
 ccaagggtt tcatggctt cactgtcaaa tcaacttc当地 tgggtctt当地 taatctcaa 240
 agtcttc当地 atcttc当地 aactcaactt atgc当地 cccccccaaa aaaaactgaa aatattcaag 300
 tcccttgatg atttggctag gaacaatgtt tgattc当地 tcaaatctg cgagaatct 360
 tggcaaccc aagaactactt gccc当地 gatccg gtgtc当地 gagcgttccggg gcaagtgc当地 420
 gagttgaggg aaaggccaa ggagatccccc gacgactattt tggtgggtt agttggagat 480
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 aaggatgaga ctggggctgaa gccc当地 gtggcaatgtt ggacttagggg atggactgccc 600
 gaagagaata qacatgtt当地 ccttctcaat aagtactttt atttgc当地 aagggttgat 660
 atgaggaaaa ttgagaagac tattcaatc ctcatcgctt cggaaatggaa tatcaatgtt当地 720
 gaaaacagcc cctatcttggg acatccccc当地 aagagagac aaccttccata 780
 tcccatccaa acacagccaa gctggccaa cactacggcc acaagaaactt cgctccatc 840
 tgc当地 cccca tggccctt当地 cggagggccg caccggccacg cttacacccaa gatcggtggaa 900
 aagctcgctt当地 agatcgccccc当地 gacacacaaa gtaattgtt当地 ttgc当地 gatgc当地 960
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 <211> 394
 <212> PRT
 <213> Hedera helix

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 Phe Met Ala Ser Thr Val Asn Ser Asn Ser Met Val Leu Asp Asn Leu
 35 40 45
 Lys Ser Pro Pro Asn Leu Gln Val Thr His Ser Met Pro Pro Gln Lys
 50 55 60
 Leu Glu Ile Phe Lys Ser Leu Asp Asp Trp Ala Arg Asn Asn Val Leu
 65 70 75 80
 Ile His Leu Lys Ser Val Glu Lys Ser Trp Gln Pro Gln Asp Tyr Leu
 85 90 95
 Pro Asp Pro Val Ser Asp Gly Phe Glu Glu Gln Val Arg Glu Leu Arg
 100 105 110
 Glu Arg Ala Lys Glu Ile Pro Asp Asp Tyr Phe Val Val Leu Val Gly
 115 120 125
 Asp Met Ile Thr Glu Glu Ala Leu Pro Thr Tyr Met Ser Met Leu Asn
 130 135 140

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Arg Cys Asp Gly Ile Lys Asp Glu Thr Gly Ala Glu Pro Ser Ala Trp
145 150 155 160

Ala Met Trp Thr Arg Ala Trp Thr Ala Glu Glu Asn Arg His Gly Asp
165 170 175

Leu Leu Asn Lys Tyr Leu Tyr Leu Ser Gly Arg Val Asp Met Arg Lys
180 185 190

Ile Glu Lys Thr Ile Gln Tyr Leu Ile Gly Ser Gly Met Asp Ile Lys
195 200 205

Ser Glu Asn Ser Pro Tyr Leu Gly Phe Ile Tyr Thr Ser Phe Gln Glu
210 215 220

Arg Ala Thr Phe Ile Ser His Ala Asn Thr Ala Lys Leu Ala Gln His
225 230 235 240

Tyr Gly Asp Lys Asn Leu Ala His Ile Cys Gly Ser Ile Ala Ser Asp
245 250 255

Glu Lys Arg His Ala Thr Ala Tyr Thr Lys Ile Val Glu Lys Leu Ala
260 265 270

Glu Ile Asp Pro Asp Thr Thr Val Ile Ala Phe Ala Asp Met Met Arg
275 280 285

Lys Lys Ile Thr Met Pro Ala His Leu Met Tyr Asp Gly Ser Asp Glu
290 295 300

Leu Leu Phe Lys His Phe Thr Ala Val Ala Gln Arg Val Gly Val Tyr
305 310 315 320

Ser Ala Leu Asp Tyr Cys Asp Ile Leu Glu Phe Leu Val Asp Lys Trp
325 330 335

Asn Val Glu Arg Leu Thr Gly Leu Ser Asp Glu Gly Arg Lys Ala Gln
340 345 350

Glu Tyr Val Cys Glu Leu Gly Pro Lys Ile Arg Arg Val Glu Glu Lys
355 360 365

Val Gln Gly Lys Glu Lys Lys Lys Ala Glu His Pro Val Ser Phe
370 375 380

Ser Trp Ile Phe Asn Arg Glu Leu Lys Ile
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<211> 28

<212> DNA

<213> Artificial Sequence

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<223> PCR primer

<400> 11

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<210> 12
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR primer

<400> 12
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27

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